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Sequence Listing was accepted.

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Timestamp: [year=2008; month=11; day=21; hr=15; min=10; sec=50; ms=125;
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Application No: 10576995

Version No: 1.0

Input Set:

Output Set:

Started: 2008-10-29 16:17:57.183

Finished: 2008-10-29 16:17:57.842

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 659 ms

Total Warnings: 7

Total Errors: 0

No. of SeqIDs Defined: 8

Actual SeqID Count: 8

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)

SEQUENCE LISTING

<110> HUI, MIZHOU

<120> A NOVEL CHIMERIC POLYPEPTIDE AND USE THEREOF

<130> 50001-003US1

<140> 10576995

<141> 2008-10-29

<150> PCT/US2004/027655

<151> 2004-08-25

<150> 60/497,988

<151> 2003-08-26

<160> 8

<170> PatentIn version 3.5

<210> 1

<211> 1923

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
construct

<400> 1

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cacgccttgc ccgccaggt ggcatttaca cctacgccc cggagcccg gagcacatgc	120
cggctcagag aatactatga ccagacagct cagatgtgct gcagcaaag ctgcgcgggc	180
caacatgcaa aagtcttctg taccaagacc tcggacaccg tgtgtgactc ctgtgaggac	240
agcacataca ccagctctg gaactgggtt cccgagtgtc tgagctgtgg ctcccgtgt	300
agctctgacc aggtggaac tcaagcctgc actcgggaac agaaccgat ctgcacctgc	360
aggcccggt ggtactgctg gctgagcaag caggaggggt gccggtgtg cgcgcgctg	420
cgcaagtgcc gcccggtt cggcgtggcc agaccaggaa ctgaaacatc agacgtggtg	480
tgcaagccct gtgccccggg gacgttctcc aacacgactt catccacgga tatttgcagg	540
ccccaccaga tctgtaacgt ggtggccatc cctgggaatg caagcatgga tgcagtctgc	600
acgtccacgt cccccaccg gagtatggcc ccaggggcag tacacttacc ccagccagtg	660
tccacacgat cccaacacac gcagccaact ccagaacca gcactgctcc aagcacctcc	720
ttctgtctcc caatgggcc cagccccca gctgaaggga gcactggcga cgagcccaaa	780

tcttgtgaca aaactcacac atgccaccg tgcccagcac ctgaactcct ggggggaccg	840
tcagtcttcc tcttcccccc aaaaccaag gacaccctca tgatctcccg gaccctgag	900
gtcacatgcg tgggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac	960
gtggacggcg tggaggtgca taatgccaaag acaaagccgc gggaggagca gtacaacagc	1020
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag	1080
tacaagtgca aggtctccaa caaagccctc ccagcccca tcgagaaaac catctccaaa	1140
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg	1200
accaagaacc aggtcagcct gacctgctg gtcaaaggct tctatcccag cgacatcgcc	1260
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccggtgtg	1320
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag	1380
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag	1440
aagagcctct cctgtctctc gggtaaacga ccctctggga gaaaatccag caagatgcaa	1500
gccttcagaa tctgggatgt taaccagaag accttctatc tgaggaacaa ccaactagtt	1560
gctggatact tgcaaggacc aaatgtcaat ttaaaagaaa agatagatgt ggtaccatt	1620
gagcctcatg ctctgttctt gggaatccat ggagggaaga tgtgcctgtc ctgtgtcaag	1680
tctggtgatg agaccagact ccagctggag gcagttaaca tctactgacct gagcgagaac	1740
agaaagcagg acaagcgctt cgcttcctc cgctcagaca gtggcccccac caccagtttt	1800
gagtctgccg cctgcccccg ttggttcctc tgcacagcga tggaagctga ccagcccgtc	1860
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gag	1923

<210> 2

<211> 619

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
construct

<400> 2

Leu	Pro	Ala	Gln	Val	Ala	Phe	Thr	Pro	Tyr	Ala	Pro	Glu	Pro	Gly	Ser
1				5					10					15	

Thr	Cys	Arg	Leu	Arg	Glu	Tyr	Tyr	Asp	Gln	Thr	Ala	Gln	Met	Cys	Cys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20

25

30

Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
 35 40 45

Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
 50 55 60

Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
 65 70 75 80

Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
 85 90 95

Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
 100 105 110

Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
 115 120 125

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
 130 135 140

Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
 145 150 155 160

Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
 165 170 175

Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
 180 185 190

His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
 195 200 205

Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
 210 215 220

Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Glu Pro Lys Ser Cys
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys Arg Pro Ser Gly Arg Lys Ser Ser Lys Met Gln Ala Phe
465 470 475 480

Arg Ile Trp Asp Val Asn Gln Lys Thr Phe Tyr Leu Arg Asn Asn Gln
 485 490 495

Leu Val Ala Gly Tyr Leu Gln Gly Pro Asn Val Asn Leu Lys Glu Lys
 500 505 510

Ile Asp Val Val Pro Ile Glu Pro His Ala Leu Phe Leu Gly Ile His
 515 520 525

Gly Gly Lys Met Cys Leu Ser Cys Val Lys Ser Gly Asp Glu Thr Arg
 530 535 540

Leu Gln Leu Glu Ala Val Asn Ile Thr Asp Leu Ser Glu Asn Arg Lys
 545 550 555 560

Gln Asp Lys Arg Phe Ala Phe Ile Arg Ser Asp Ser Gly Pro Thr Thr
 565 570 575

Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp Phe Leu Cys Thr Ala Met
 580 585 590

Glu Ala Asp Gln Pro Val Ser Leu Thr Asn Met Pro Asp Glu Gly Val
 595 600 605

Met Val Thr Lys Phe Tyr Phe Gln Glu Asp Glu
 610 615

<210> 3
 <211> 235
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 construct

<400> 3
 Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
 1 5 10 15

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
 20 25 30

Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
 35 40 45

Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
50 55 60

Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
65 70 75 80

Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
85 90 95

Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
100 105 110

Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
115 120 125

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
130 135 140

Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
145 150 155 160

Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
165 170 175

Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
180 185 190

His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
195 200 205

Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
210 215 220

Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp
225 230 235

<210> 4

<211> 231

<212> PRT

<213> Homo sapiens

<400> 4

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

1	5	10	15
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro	20	25	30
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val	35	40	45
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val	50	55	60
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln	65	70	75
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln	85	90	95
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala	100	105	110
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro	115	120	125
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr	130	135	140
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser	145	150	155
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr	165	170	175
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr	180	185	190
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe	195	200	205
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys	210	215	220
Ser Leu Ser Leu Ser Pro Gly	225	230	

<210> 5
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
construct

<400> 5
Arg Pro Ser Gly Arg Lys Ser Ser Lys Met Gln Ala Phe Arg Ile Trp
1 5 10 15

Asp Val Asn Gln Lys Thr Phe Tyr Leu Arg Asn Asn Gln Leu Val Ala
20 25 30

Gly Tyr Leu Gln Gly Pro Asn Val Asn Leu Lys Glu Lys Ile Asp Val
35 40 45

Val Pro Ile Glu Pro His Ala Leu Phe Leu Gly Ile His Gly Gly Lys
50 55 60

Met Cys Leu Ser Cys Val Lys Ser Gly Asp Glu Thr Arg Leu Gln Leu
65 70 75 80

Glu Ala Val Asn Ile Thr Asp Leu Ser Glu Asn Arg Lys Gln Asp Lys
85 90 95

Arg Phe Ala Phe Ile Arg Ser Asp Ser Gly Pro Thr Thr Ser Phe Glu
100 105 110

Ser Ala Ala Cys Pro Gly Trp Phe Leu Cys Thr Ala Met Glu Ala Asp
115 120 125

Gln Pro Val Ser Leu Thr Asn Met Pro Asp Glu Gly Val Met Val Thr
130 135 140

Lys Phe Tyr Phe Gln Glu Asp Glu
145 150

<210> 6
<211> 1467
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
construct

<400> 6

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cggctcagag	aatactatga	ccagacagct	cagatgtgct	gcagcaaatg	ctcgccgggc	180
caacatgcaa	aagtcttctg	taccaagacc	tcggacaccg	tgtgtgactc	ctgtgaggac	240
agcacataca	cccagctctg	gaactgggtt	cccagtgct	tgagctgtgg	ctcccgtgt	300
agctctgacc	aggtggaac	tcaagcctgc	actcgggaac	agaaccgcat	ctgcacctgc	360
agggccggct	ggtactgcgc	gctgagcaag	caggaggggt	gccggtgtg	cgcgccgtg	420
cgcaagtgcc	gcccgggctt	cggcgtggcc	agaccaggaa	ctgaaacatc	agacgtggtg	480
tgcaagccct	gtgccccggg	gacgttctcc	aacacgactt	catccacgga	tatttgcagg	540
ccccaccaga	tctgtaacgt	ggtggccatc	cctgggaatg	caagcatgga	tgcagtctgc	600
acgtccacgt	ccccacccg	gagtatggcc	ccaggggcag	tacacttacc	ccagccagtg	660
tccacacgat	cccaacacac	gcagccaact	ccagaacca	gcactgctcc	aagcacctcc	720
ttctgctcc	caatgggccc	cagcccccca	gctgaaggga	gcactggcga	cgagcccaa	780
tcttgtgaca	aaactcacac	atgccaccg	tgcccagcac	ctgaactcct	ggggggaccg	840
tcagtcttcc	tcttcccccc	aaaaccaag	gacacctca	tgatctcccg	gaccttgag	900
gtcacatgcy	tgggtgtgga	cgtgagccac	gaagacctg	aggtcaagtt	caactggtac	960
gtggacggcg	tggaggtgca	taatgccaa	acaaagccgc	gggaggagca	gtacaacagc	1020
acgtaccgtg	tggtcagcgt	cctcaccgtc	ctgcaccagg	actggctgaa	tggcaaggag	1080
tacaagtgca	aggtctccaa	caaagccctc	ccagccccca	tcgagaaaac	catctccaaa	1140
gccaaagggc	agccccgaga	accacaggtg	tacacctgc	ccccatcccg	ggatgagctg	1200
accaagaacc	aggtcagcct	gacctgcctg	gtcaaaggct	tctatcccag	cgacatcgcc	1260
gtggagtggg	agagcaatgg	gcagccggag	aacaactaca	agaccacgcc	tcccgtgctg	1320
gactccgacg	gtctcttctt	cctctacagc	aagctcaccg	tggacaagag	caggtggcag	1380
caggggaacg	tcttctcatg	ctccgtgatg	catgaggctc	tgcacaacca	ctacacgcag	1440
aagagcctct	cctgtctcc	gggtaaa				1467

<210> 7

<211> 467

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
construct

<400> 7

Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
1 5 10 15

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
20 25 30

Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
35 40 45

Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
50 55 60

Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
65 70 75 80

Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
85 90 95

Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
100 105 110

Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
115 120 125

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
130 135 140

Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
145 150 155 160

Gln Ile Cys Asn Val Val Ala Ile Pro Gly